1600

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/726,348A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

Does Not Comply
Corrected Diskette Needed

Error on p. 3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/726,348A

DATE: 08/22/2002
TIME: 16:35:19

Input Set : A:\Subst SEQ LIST CRF.txt
Output Set: N:\CRF4\08222002\I726348A.raw

<110> APPLICANT: Wei, Ying-Fei et al.

<120> TITLE OF INVENTION: Transforming Growth Factor Alpha HIII

<130> FILE REFERENCE: PF220P1

<140> CURRENT APPLICATION NUMBER: 09/726,348A
<141> CURRENT FILING DATE: 2000-12-01

<150> PRIOR APPLICATION NUMBER: 08/778,545
<151> PRIOR FILING DATE: 1997-01-03

<150> PRIOR APPLICATION NUMBER: 60/011,136
<151> PRIOR FILING DATE: 1996-01-04

<150> PRIOR APPLICATION NUMBER: 60/168,387
<151> PRIOR FILING DATE: 1999-12-02

<160> NUMBER OF SEQ ID NOS: 21

<170> SOFTWARE: PatentIn version 3.0

<210> SEQ ID NO: 1
<211> LENGTH: 923
<212> TYPE: DNA
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 1

gaaaatggcg cctcacggcc cgggtagtct tacgaccctg gtgccctggg ctgccgccct 60
gctcctcgct ctgggcgtgg aaagggctct ggcgctaccc gagatatgca cccaatgtcc 120
agggagcgtg caaaatttgt caaaagtggc cttttattgt aaaacgacac gagagctaat 180
gctgcatgcc cgttgctgcc tgaatcagaa gggcaccatc ttggggctgg atctccagaa 240
ctgttctctg gaggaccctg gtccaaactt tcatcaggca cataccactg tcatcataga 300
cctgcaagca aacccccctca aaggtgactt ggccaacacc ttccgtggct ttactcagct 360
ccagactctg atactgccac aacatgtcaa ctgtcctgga ggaattaatg cctggaatac 420
tatcacctct tatatagaca accaaatctg tcaagggcaa aagaaccttt gcaataacac 480
tggggaccca gaaatgtgtc ctgagaatgg atcttgtgta cctgatggtc caggtctttt 540
gcagtgtgtt tgtgctgatg gtttccatgg atacaagtgt atgcgccagg gctcgttctc 600
actgcttatg ttcttcggga ttctgggagc caccactcta tccgtctcca ttctgctttg 660
ggcgacccag cgccgaaaag ccaagacttc atgaactaca taggtcttac cattgaccta 720
agatcaatct gaactatctt agcccagtca gggagctctg cttcctagaa aggcatcttt 780
cgccagtgga ttcgcctcaa ggttgaggcc gccattggaa gatgaaaaat tgcactccct 840
tggtgtagac aaataccagt tcccattggt gttgttgcct ataataaaca ctttttttctt 900
ttttaaaaaa aaaaaaaaaa aaa 923

<210> SEQ ID NO: 2
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: homo sapiens

<400> SEQUENCE: 2

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro Trp Ala
-25 -20 -15 -10
Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala Leu Pro
-5 1 5

RAW SEQUENCE LISTING
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Input Set : A:\Subst SEQ LIST CRF.txt
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Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn Leu Ser Lys Val
10 15 20
Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala Arg Cys
25 30 35
Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln Asn Cys
40 45 50 55
Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr Thr Val
60 65 70
Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala Asn Thr
75 80 85
Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln His Val
90 95 100
Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile
105 110 115
Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn Thr Gly
120 125 130 135
Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp Gly Pro
140 145 150
Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr Lys Cys
155 160 165
Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile Leu Gly
170 175 180
Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln Arg Arg
185 190 195
Lys Ala Lys Thr Ser
200

<210> SEQ ID NO: 3
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: homo sapiens
<400> SEQUENCE: 3
Gly Gln Lys Asn Leu Cys Asn Asn Thr Gly Asp Pro Glu Met Cys Pro
1 5 10 15
Glu Asn Gly Ser Cys Val Pro Asp Gly Pro Gly Leu Leu Gln Cys Val
20 25 30
Cys Ala Asp Gly Phe His Gly Tyr Lys Cys Met Arg Gln Gly Ser Phe
35 40 45
Ser Leu Leu Met
50

<210> SEQ ID NO: 4
<211> LENGTH: 733
<212> TYPE: DNA
<213> ORGANISM: homo sapiens
<400> SEQUENCE: 4
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60
aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120
tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300

RAW SEQUENCE LISTING DATE: 08/22/2002
PATENT APPLICATION: US/09/726,348A TIME: 16:35:19

Input Set : A:\Subst SEQ LIST CRF.txt
Output Set: N:\CRF4\08222002\I726348A.raw

```
    151 ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg    360
    153 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc    420
    155 catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct    480
    157 atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga    540
    159 ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg    600
    161 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc    660
    163 acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc    720
    165 gactctagag gat                                                     733
    168 <210> SEQ ID NO: 5
    169 <211> LENGTH: 5
    170 <212> TYPE: PRT
    171 <213> ORGANISM: WSXWS motif
    173 <220> FEATURE:
    174 <221> NAME/KEY: SITE
    175 <222> LOCATION: (3)..(3)
    176 <223> OTHER INFORMATION: Xaa equals any amino acid
    179 <400> SEQUENCE: 5
W--> 181 Trp Ser Xaa Trp Ser
    182 1               5
    184 <210> SEQ ID NO: 6
    185 <211> LENGTH: 86
    186 <212> TYPE: DNA
    187 <213> ORGANISM: oligonucleotide
    189 <220> FEATURE:
    190 <221> NAME/KEY: protein_bind
    191 <222> LOCATION: (1)..(86)
    192 <223> OTHER INFORMATION: 5' primer containing 18bp complementary to SV40 promotor and
    193       an XhoI site
    196 <400> SEQUENCE: 6
    197 gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc     60
    199 cccgaaatat ctgccatctc aattag                                        86
    202 <210> SEQ ID NO: 7
    203 <211> LENGTH: 27
    204 <212> TYPE: DNA
    205 <213> ORGANISM: oligonucleotide
    207 <220> FEATURE:
    208 <221> NAME/KEY: protein_bind
    209 <222> LOCATION: (1)..(27)
    210 <223> OTHER INFORMATION: 3' primer containing sequence complementary to SV40
    211       promotor and a HindIII site
    214 <400> SEQUENCE: 7
    215 gcggcaagct ttttgcaaag cctaggc                                       27
    218 <210> SEQ ID NO: 8
    219 <211> LENGTH: 271
    220 <212> TYPE: DNA
    221 <213> ORGANISM: Homo sapiens
    223 <400> SEQUENCE: 8
    224 ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg     60
    226 aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc    120
```

Invalid response, see error summary sheet item 10

RAW SEQUENCE LISTING
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Input Set : A:\Subst SEQ LIST CRF.txt
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228 gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
230 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
232 ttttggaggc ctaggctttt gcaaaaagct t 271
235 <210> SEQ ID NO: 9
236 <211> LENGTH: 32
237 <212> TYPE: DNA
238 <213> ORGANISM: oligonucleotide
240 <220> FEATURE:
241 <221> NAME/KEY: primer_bind
242 <222> LOCATION: (1)..(32)
243 <223> OTHER INFORMATION: 5' PCR primer
246 <400> SEQUENCE: 9
247 gcgctcgagg gatgacagcg atagaacccc gg 32
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 31
252 <212> TYPE: DNA
253 <213> ORGANISM: oligonucleotide
255 <220> FEATURE:
256 <221> NAME/KEY: primer_bind
257 <222> LOCATION: (1)..(31)
258 <223> OTHER INFORMATION: 3' PCR primer
261 <400> SEQUENCE: 10
262 gcgaagcttc gcgactcccc ggatccgcct c 31
265 <210> SEQ ID NO: 11
266 <211> LENGTH: 12
267 <212> TYPE: DNA
268 <213> ORGANISM: oligonucleotide
270 <220> FEATURE:
271 <221> NAME/KEY: primer_bind
272 <222> LOCATION: (1)..(12)
273 <223> OTHER INFORMATION: NF-KB repeat in upstream primer
276 <400> SEQUENCE: 11
277 ggggactttc cc 12
280 <210> SEQ ID NO: 12
281 <211> LENGTH: 73
282 <212> TYPE: DNA
283 <213> ORGANISM: oligonucleotide
285 <220> FEATURE:
286 <221> NAME/KEY: primer_bind
287 <222> LOCATION: (1)..(73)
288 <223> OTHER INFORMATION: 5' primer containing the NF-KB binding site, 18bp
289 complementary to SV40 promotor, and an XhoI site
292 <400> SEQUENCE: 12
293 gcggcctcga ggggactttc ccggggactt tccgggact ttccatcctg 60
295 ccatctcaat tag 73
298 <210> SEQ ID NO: 13
299 <211> LENGTH: 256
300 <212> TYPE: DNA
301 <213> ORGANISM: Homo sapiens

RAW SEQUENCE LISTING DATE: 08/22/2002
PATENT APPLICATION: US/09/726,348A TIME: 16:35:19

Input Set : A:\Subst SEQ LIST CRF.txt
Output Set: N:\CRF4\08222002\I726348A.raw

303 <400> SEQUENCE: 13
304 ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60
306 caattagtca gcaaccatag tcccgccccc aactccgccc atcccgcccc taactccgcc 120
308 cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
310 ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggctttttttg gaggcctagg 240
312 cttttgcaaa aagctt 256
315 <210> SEQ ID NO: 14
316 <211> LENGTH: 27
317 <212> TYPE: DNA
318 <213> ORGANISM: oligonucleotide
320 <220> FEATURE:
321 <221> NAME/KEY: primer_bind
322 <222> LOCATION: (1)..(27)
323 <223> OTHER INFORMATION: 5' primer containing a BamHI site and 18nt of TGF alpha HIII
326 <400> SEQUENCE: 14
327 cgcggatccg ggcaaaagaa cctttgc 27
330 <210> SEQ ID NO: 15
331 <211> LENGTH: 30
332 <212> TYPE: DNA
333 <213> ORGANISM: oligonucleotide
335 <220> FEATURE:
336 <221> NAME/KEY: primer_bind
337 <222> LOCATION: (1)..(30)
338 <223> OTHER INFORMATION: 3' primer containing an XbaI site and 21 nt of TGF alpha HIII
341 <400> SEQUENCE: 15
342 gcgtctagac taaagcagtg agaacgagcc 30
345 <210> SEQ ID NO: 16
346 <211> LENGTH: 34
347 <212> TYPE: DNA
348 <213> ORGANISM: oligonucleotide
350 <220> FEATURE:
351 <221> NAME/KEY: primer_bind
352 <222> LOCATION: (1)..(34)
353 <223> OTHER INFORMATION: 5' primer containing a BamHI site
356 <400> SEQUENCE: 16
357 cgcggatccg tccatcatgg cgcctcacgg cccg 34
360 <210> SEQ ID NO: 17
361 <211> LENGTH: 33
362 <212> TYPE: DNA
363 <213> ORGANISM: oligonucleotide
365 <220> FEATURE:
366 <221> NAME/KEY: primer_bind
367 <222> LOCATION: (1)..(33)
368 <223> OTHER INFORMATION: 3' primer containing an XbaI site
371 <400> SEQUENCE: 17
372 gcgtctagac tacataagca gtgacaacga gcc 33
375 <210> SEQ ID NO: 18
376 <211> LENGTH: 28
377 <212> TYPE: DNA

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/22/2002
PATENT APPLICATION: US/09/726,348A TIME: 16:35:20

Input Set : A:\Subst SEQ LIST CRF.txt
Output Set: N:\CRF4\08222002\I726348A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 3

DATE: 08/22/2002
TIME: 16:35:20

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/726,348A

Input Set : A:\Subst SEQ LIST CRF.txt
Output Set: N:\CRF4\08222002\I726348A.raw

:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0